

A. Saoud

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/349,954

DATE: 09/22/2000

TIME: 13:10:37

Input Set : A:\PTO.txt

Output Set: N:\CRF3\09222000\I349954.raw

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3 <110> APPLICANT: Hayward, Nicholas K.
4   Weber, Gunther
5   Grimmond, Sean
6   Nordenskjold, Magnus
7   Larsson, Catharina
9 <120> TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
10  SAME
12 <130> FILE REFERENCE: Dav. Col. Cave
14 <140> CURRENT APPLICATION NUMBER: 09/349,954
15 <141> CURRENT FILING DATE: 1999-07-08
17 <150> PRIOR APPLICATION NUMBER: 08/765,588
18 <151> PRIOR FILING DATE: 1996-02-22
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 649
26 <212> TYPE: DNA
27 <213> ORGANISM: Nucleotide Sequence of VEGF165
29 <220> FEATURE:
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31 <222> LOCATION: (17)..(589)
33 <400> SEQUENCE: 1
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37           1           5           10
39 gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100
41 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
42           15           20           25
44 atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148
46 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
47           30           35           40
49 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196
51 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
52 45           50           55           60
54 atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244
56 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
57           65           70           75
59 tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292
61 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
62           80           85           90
64 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
66 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
67           95           100          105
69 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag 388
71 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
72           110          115          120
74 cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436

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76 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
77 125          130          135          140
79 aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa 484
81 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
82          145          150          155
84 gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc 532
86 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
87          160          165          170
89 aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag 580
91 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
92          175          180          185
94 ccg agg cgg /tgagccgggc aggaggaagg agcctccctc agcgtttcgg 629
96 Pro Arg Arg
97          190
99 gaaccagatc tctcaccagg 649
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 191
105 <212> TYPE: PRT
106 <213> ORGANISM: Nucleotide Sequence of VEGF165
108 <400> SEQUENCE: 2
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110 1          5          10          15
112 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
113          20          25          30
115 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
116          35          40          45
118 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
119          50          55          60
121 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
122 65          70          75          80
124 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
125          85          90          95
127 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
128          100          105          110
130 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
131          115          120          125
133 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
134          130          135          140
136 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
137 145          150          155          160
139 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
140          165          170          175
142 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
143          180          185          190
146 <210> SEQ ID NO: 3
147 <211> LENGTH: 1094
148 <212> TYPE: DNA
149 <213> ORGANISM: Nucleotide Sequence of SOM175
151 <220> FEATURE:

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152 <221> NAME/KEY: CDS
153 <222> LOCATION: (3)..(623)
155 <400> SEQUENCE: 3
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158 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
159 1 5 10 15
161 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
163 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
164 20 25 30
166 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
168 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
169 35 40 45
171 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
173 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
174 50 55 60
176 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
178 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
179 65 70 75
181 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
183 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
184 80 85 90 95
186 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
188 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
189 100 105 110
191 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
193 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
194 115 120 125
196 aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac 431
198 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
199 130 135 140
201 cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca 479
203 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
204 145 150 155
206 ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
208 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
209 160 165 170 175
211 gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc 575
213 Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
214 180 185 190
216 gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct 623
218 Ala Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
219 195 200 205
221 tagagctcaa cccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683
224 agactcagca ggggtgacttg cctcagagcc tatatcccag tggggggaaca aaggggagcc 743
227 tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
230 ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
233 agagttggaa gaggagactg ggagggcagca agaggggtca cataccagct caggggagaa 923
236 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcatcttaca actggctctt 983
239 cctcccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tggtaacaaga 1043

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242 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a      1094
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247 <211> LENGTH: 207
248 <212> TYPE: PRT
249 <213> ORGANISM: Nucleotide Sequence of SOM175
251 <400> SEQUENCE: 4
252 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
253   1           5           10           15
255 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
256           20           25           30
258 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
259           35           40           45
261 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
262           50           55           60
264 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
265           65           70           75           80
267 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
268           85           90           95
270 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
271           100          105          110
273 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
274           115          120          125
276 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
277           130          135          140
279 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
280           145          150          155          160
282 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
283           165          170          175
285 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
286           180          185          190
288 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
289           195          200          205
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293 <211> LENGTH: 993
294 <212> TYPE: DNA
295 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
297 <220> FEATURE:
298 <221> NAME/KEY: CDS
299 <222> LOCATION: (3)..(566)
301 <400> SEQUENCE: 5
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304   Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
305   1           5           10           15
307 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac      95
309 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
310           20           25           30
312 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc      143
314 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
315           35           40           45

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317 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
319 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
320      50      55      60
322 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
324 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
325      65      70      75
327 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
329 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
330      80      85      90      95
332 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
334 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
335      100      105      110
337 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
339 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
340      115      120      125
342 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
344 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
345      130      135      140
347 cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479
349 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
350      145      150      155
352 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527
354 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
355      160      165      170      175
357 ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576
359 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
360      180      185
362 cttttcagac tcagcagggt gacttgctc agaggctata tccagtgagg ggaacaaagg 636
365 ggagcctggt aaaaaacagc caagcccccag agacctcagc ccaggcagaa gctgctctag 696
368 gacctgggcc tctcagaggg ctcttctgcc atcccttgtc tccctgaggg catcatcaaa 756
371 caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816
374 ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876
377 gctcttctc cctcactaa gaagacccaa acctctgcat aatgggattt gggctttggt 936
380 acaagaactg tgaccccaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa 993
384 <210> SEQ ID NO: 6
385 <211> LENGTH: 188
386 <212> TYPE: PRT
387 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
389 <400> SEQUENCE: 6
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391      1      5      10      15
393 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
394      20      25      30
396 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
397      35      40      45
399 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
400      50      55      60
402 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
403      65      70      75      80

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VERIFICATION SUMMARY

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L:788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:793 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16